

FIG. 1

Consensus	90
BDV JCT	90
BDV Briese	90
GTTGCCTTAAACAACCAACATCATYATYCTTCTARCAAAATGAACACACGCAATGCCACCCAGAGAGCGCTGTTGATGACGCCGATGA...T.C.....C...C.T.....	
Consensus	180
BDV JCT	180
BDV Briese	180
CCATGGAGGAYCAAGATYATATGAACCCCGAGCGCTCCCYAAGCTCCCYGGRAATTCTTACAATACACCGTTGGGGGCTCTGACCC.....T.....T.....C.....T.....G.....	
Consensus	270
BDV JCT	270
BDV Briese	270
CGCATCGGGTATAGGCATGAGAARGATCAGGCAGAACCGAGTGGCATTTGTAGACCATCAGCGCGGATATGTTTCAACAGATAAG.T.....T.....A.C.....C.....	
Consensus	360
BDV JCT	360
BDV Briese	360
CGCCYAGCCTTGTGTTCTATGTTGCTAATCCAGGACTGCACGCTGCGTTTGTTCAGGGAGGGTCCCTCGTGAATCYTACCTGTGCGAC.....T.....T.....C.....	
Consensus	450
BDV JCT	450
BDV Briese	450
CGCCTGTACGCGTGGGAACAGACTGTGTAAAGACTGCRAAGTTTACGGGGAAAGACRACRACGCGTGATCTCACCGAGCTGGAGAT.....C.....A.....G.....T.....A.....G.....	
Consensus	540
BDV JCT	540
BDV Briese	540
TCTCCTCTATMTTCAGCCATGTTGCTCATTACTAATWGGGTTGTGATAGGATCGTCTCTTAAGATYAAAGCAGGAGCCGAGCAGATCAA.....T.....C.....A.....G.....C.....	
Consensus	630
BDV JCT	630
BDV Briese	630
AGAAAAGGTTTAAACTATGATGGCAGCCTTAAACCGGCCATCCCATGGTGAGACTGTACACTACTYACAGATGTTTAAATCCACATGAGGT.....C.....	

FIG. 2A

Consensus	CTATACATTGGATTAAAGCCCAACCCCTGGGTAGGCTCCTTTTGTGTCCTACTAATACAGACTTTGAGTCCCCAGGTAAGAATTYA	720
BDV JCTG.....A.....	720
BDV BrieseA.....T.....	720
Consensus	TGGAYCAGATTAAACCTTTGTCGCAAGTTATGCRCAAGATGACTACGTACACTACTATAAAGGAGTACCTGCAGAAATGYATGGATGCTACCC	810
BDV JCTT.....A.....G.....	810
BDV BrieseC.....G.....A.....T.....C.....	810
Consensus	TTACAATCCCYGTAGTTGCATATGAGATYCGTGACTTTTGAAGTTTCAGCAAGCTTAARGAGGAWCATGCTGACCTGTTTCCGTTTC	900
BDV JCTT.....T.....C.....	900
BDV BrieseC.....C.....G.....T.....C.....T.....	900
Consensus	TGGGGCYATTMGRCAACCCCGGCTATCAAGCTKGGCCGACGAGCTTTCCCAATCTGGCYTCYGCAGCGTTTACTGGAGTAAGAAGG	990
BDV JCTT.....C.....G.....	990
BDV BrieseC.....A.....G.....A.....C.....C.....	990
Consensus	ARAAYCCCACAATGGCRGGCTACCGGGCCCTCCACCATCCAGCCGGCGCRAGTGTCAAGGARACCCAGCTTGCCCGGTATAGCGCGCGCG	1080
BDV JCTG.....T.....G.....	1080
BDV BrieseA.....C.....A.....G.....A.....	1080
Consensus	AGATATCTCGYGGRGARGACGGGGCAGAGCTCTCAGGTGAGATCTCTGCCATATGARRATGATAGTGTGACTGGTCTAAACTARAAA	1170
BDV JCTC.....G.....A.....	1170
BDV BrieseT.....A.....G.....AG.....A.....	1170
Consensus	CAATGAACAAACCAATAAATAAATGCGGCAACCCYCCGACCTGYGATGAGYTCGACCTCCCGGTGACATTTGCTTGAAYTAGT	1260
BDV JCTT.....C.....T.....	1260
BDV BrieseT.....C.....C.....C.....	1260
Consensus	CAGGAGGCTCAATGGCAACGSGACCCATCGAGTCTGTGTCGACTCCCTGGAGACGAAGAAGATCCCCAGACACTACGACGGGAACGAYCGG	1350
BDV JCTG.....C.....	1350
BDV BrieseC.....T.....C.....	1350

FIG. 2B

Consensus	GGTCACCAAGACACCGGAAGRTCCCAAGGAATGCATTGACCCCAACCRGTAGACCACTCCTGAAGGACCTCAGGAAGAACCCTCCATGA	1440
BDV JCTA.....G.....	1440
BDV BrieseG.....A.....	1440
Consensus	TCTCAGACCCAGACAGCGAACCAGGAGGAGCTRTCGAATGATGAGCTWATCAAGAAGYTAGTGACGGAGCTGGCCGAGATAGCA	1530
BDV JCTA.....G.....T.....C.....	1530
BDV BrieseA.....G.....A.....T.....	1530
Consensus	TGATCGAGGTGAGGAGGTCCGGGCACTCTTGGRGACATCTCGGCTCGYATCGAGSCAGGTTTGAGTCCCTGTCCGCCCTCCAAGTGG	1620
BDV JCTG.....A.....C.....T.....	1620
BDV BrieseA.....T.....	1620
Consensus	AAACCATCCAGACAGCTCAGCGGTGCGAYCACCTCGAYAGCATCAGRATCCTYGGCGAGAACATCAAGATACTRGATCGCTCCATGAGA	1710
BDV JCTC.....T.....A.....T.....G.....	1710
BDV BrieseT.....C.....G.....C.....A.....	1710
Consensus	CAATGATGGAGACAAATGAAGCTCATGATGGAGAGGTGGAYCTCCTTACGCATCAACCCCGTGGGACCTCTGCACCCATGTTGCCCT	1800
BDV JCTG.....C.....T.....	1800
BDV BrieseT.....	1800
Consensus	CCCATCTGCACCTCCGGCATTTATCCCAAGCTCCCAAGTGCCCGACARCGGATGARTGGGACATCATACCATAAAAAATCGAATCA	1890
BDV JCTG.....G.....A.....	1890
BDV BrieseA.....A.....	1890
Consensus	CCATGAATTCAAARCATTCCTATGTGGAGCTCAAGGRCAAGTAATCGTCCCTGGATGGCCCACTGATGCTTGAGATAGACTTTGTAG	1980
BDV JCTG.....A.....	1980
BDV BrieseA.....	1980
Consensus	GRGGGACTTCACGGAACCAAGTTCCTTAACATCCCATTTCTTTTTCAGTGAAGAGCCCTCTGCAGCTTCCACGCGAGAGAAGTTGACCCGACT	2070
BDV JCT	.A.....	2070
BDV Briese	.G.....	2070

FIG. 2C

Consensus	ACTTYACYATTGACGTAGARCCAGCAGGTCAATCCCTGGTCAAYATATACTTCCAGATTGACGACCTCTCTGCTCCTAACACTCACTCAC	2160
BDV JCT	...C.C.....G.....C.....T.....	2160
BDV Briese	...T.T.....A.....T.....	2160
Consensus	TRTCYGTTRTACAGGACCCGATTAGRAAATACATGTTCCACGGCTCACAAGAMCAGAGCAACGCAATYATGACGYTTCAATG	2250
BDV JCT	.G.C.A.....G.....A.....A.....T.....T.....	2250
BDV Briese	.A.T.G.....A.....C.....C.....C.....	2250
Consensus	TCTTYTCTATCGGCTTCGGACATTGGTGTGGYCCTCTCGGGCCCGACATTCGATCTTCAGGGCCTTAGYTGCAATACTGACTCCACT	2340
BDV JCT	...C.....C.....A.....G.....T.....C.....	2340
BDV Briese	...T.....T.....G.....C.....C.....	2340
Consensus	CCTGGAYTRATYGAICTGGAGATAAGCGACTTTCGCCACACCCCAACGGAAATGTCTATTCATGCGAGGTAGTTATCTYAAACCACAG	2430
BDV JCT	...T.A.C.T.....T.....T.....T.....	2430
BDV Briese	...C.G.T.C.....C.....C.....C.....	2430
Consensus	ACTATTAGCTCCCGGCAGTCCACACACTCATGCCCTCAAGTACCACCTGCAAAACCTATTGGGATTCCTTTGGTAGCTACAGCGGTGACCGA	2520
BDV JCT	...G.....A.....	2520
BDV Briese	...A.....	2520
Consensus	ATCATMAATCGGTACACTGGTACTGTTAAGGGTGTGTTAAACAACTACGCCAGAGGAYCCCTTCGAGTGCAACTGGTTCTACTGCTGC	2610
BDV JCT	...C.....T.....G.....T.....	2610
BDV Briese	...A.....C.....A.....C.....	2610
Consensus	TCGCGGATTACACAGAGATCTGCCGATGCTCTATTACAAATGTACGGTGGCTGTACARACATTCGCCACCGTTTCATGTAAGTGCAGTTTY	2700
BDV JCT	...A.....G.....G.....G.....	2700
BDV Briese	...G.....G.....A.....T.....	2700
Consensus	GCGACTGYAGTACGTGAGYCARCAGGAGCTAGAGAGTGGMAAGGCAATGCTGAGCGATGGCAGTACMTTAACTTATACCCCGTATATC	2790
BDV JCT seq	..G....T....T....T....G....C....C....C....C....	2790
BDV Briese	..A....C....C....C....A....A....A....A....A....	2790

FIG. 2D

Consensus	ACGCAGCTGAYCTCCTCCATACACACAGGTCTAGTAATATAAAGTCTACRGATACAGGCTCAGGCTGGGTGCACATCGGCTACCCCTCA	3600
BDV JCTC.....	3600
BDV BrieleT.....	3600
Consensus	TTTGCTTTCCTCAATCCYCTCGGGTGGCTYAGGGACCTACTTGGCTGGCGCTGGTGGTGGGGTTCCTATACCTTAATAAGTCTTTGT	3690
BDV JCTT.....	3690
BDV BrieleC.....	3690
Consensus	GTTTCCTTACCAGCTCCTTCGCGAGGAGACGCTCGGCCGCTGGCAGGAATAAACCGTACCACCAACCTCTTAAACCCCTCTTC	3780
BDV JCTT.....	3780
BDV BrieleGT.....	3780
Consensus	TCGGRACAGAGGTCTCTTCTGCTTAATCGAGYTCACCTCCGCCCATCAAGTACGAGCAYTRGGCCAGATTAAAGCAARGAACCTGGCAT	3870
BDV JCTG.....	3870
BDV BrieleA.....	3870
Consensus	CCTGTGACTATTACTTGTCTATTCGCCCAAGTTGTTATTTGCCCCCTGAAGTATATCCCATTTGGTGTYYTAAAGAGCTGCGGAGGCYATAC	3960
BDV JCTG.....	3960
BDV BrieleTC.....	3960
Consensus	TAACAGTTATAGTATCAGCTTGAAGCTGGATCAATGATGACRAAGACCCCTATATCTCTCTGTGAGATATGCACCTCACCACATCCCGGGTCC	4050
BDV JCTC.....	4050
BDV BrieleT.....	4050
Consensus	GRGCCCACTTGAGCTYCACATTGCCTACAGCGCATAGTGGTCTCTCTCTAGCCGGGARGCAGATATAGGGCCAAAGGCTTG	4140
BDV JCTC.....	4140
BDV BrieleA.....	4140
Consensus	GGATATGCTATTGCATTCATTCATTCYCTGTTATTGCCACCATACACACACACAGCTGCGCTTAATGACCTACACCACTTCTTCTGCTG	4230
BDV JCTC.....	4230
BDV BrieleT.....	4230

FIG. 2F

Consensus	CAGCAGACACAGCAAGAGCAGATGCCAYCTCCTTAATCGCCTCAGTGGTCCAGRGCCCTTTGGGARCAAGGTCATTCTTGATCAT	4320
BDV JCTC.....A.....A.....G.....	4320
BDV BrieseT.....G.....A.....	4320
Consensus	TAATCAACATGATCGACAYATTGACTCAATCAACCTCCCCCATGATTAATCAATTAAGTCTATCTYTCCTTACTCCCAAG	4410
BDV JCTC.....T.....C.....C.....	4410
BDV BrieseT.....T.....T.....T.....	4410
Consensus	GGCTTGTTATGGGAGGCAYAAATGTRTCAGTCTCCTCTGATTYGGCTCCGTATTTCRYATTCCTGAATYATGCCRCACATGACAGCT	4500
BDV JCTC.....G.....T.....A.....C.....A.....	4500
BDV BrieseT.....A.....C.....G.....T.....G.....	4500
Consensus	TACTAAAAAACTGCTYCAACTTGACCCYGTTCCTCTCATGGTCTCTTCGGTGCAGAAAGTCATGGTACTTCCCTCGAGATCCGAATGG	4590
BDV JCTT.....T.....C.....	4590
BDV BrieseC.....C.....	4590
Consensus	TYGACGGGTCACGGGAGCAGCTCCACAAGATGGGTGTCGAGCTGGARACGCCCAAGCCCTGCTGTCRTACGGCCATACCCCTCTGTCAA	4680
BDV JCTT.....G.....G.....A.....	4680
BDV BrieseC.....A.....G.....	4680
Consensus	TATTTGRCAGAGTTTATCAAAAGGCTATGCTCTCAAGAATGGCAAGTGGCGCCYGTACACCTGCTCCAGGCTGTGACAAATCCATAA	4770
BDV JCTA.....T.....C.....	4770
BDV BrieseG.....C.....	4770
Consensus	AAATGCCAGAGAGCTGGCGCGCTGGAGCCCGYRTTTGACCCGACGATGGCAGCTCTTCGMAAGGTTGTCATTCTAAGAATTGCTGACC	4860
BDV JCTG.....TG.....C.....	4860
BDV BrieseA.....CA.....A.....	4860
Consensus	TAGATATGGATCCCGACTTCAACGATATTGTTAGCGAYAAAGCGATAATCAGCTCAAGAGGGACTGGGTATTYAGTACAAATGCACRG	4950
BDV JCTC.....C.....T.....	4950
BDV BrieseT.....C.....G.....	4950

FIG. 2G

[illegible]

FIG. 2H

Consensus	TYRTACATAAATCTGCAAGCCAAAATAAYCAGCTATTAGCGGAGCGAGCAYTRGRCYVTGTACAAGCATGCTAGATTAGCTGGCCATA	5760
BDV JCT	..TG.....T.....T.G..A..TT.....	5760
BDV Briese	..CA.....C.....C.A..G..CC.....	5760
Consensus	ACCTYAAGGTAGARGAATGYTGGGTGTCAGATTCTCTGTATGAGTATGGAAGAAGCTYTTCTTCGGTGGGTACCTGTCCCGGCTGTT	5850
BDV JCT	..T.....A.....T.....C.....C.....	5850
BDV Briese	..C.....G.....C.....T.....T.....G.....	5850
Consensus	TGAAGCAGCTCTCRGSGGTGACGGAYTCYACTGGRGAGYTATTCCCAACCTATACTCAAAGTTAGCCTCTTTAACATCATCTGTGTTAA	5940
BDV JCTG.....C.C.....G..T.....	5940
BDV BrieseA.....T.T.....A..C.....G.T.....	5940
Consensus	GCGCAGCGATGCGCAGACACATCYCCATGGGTGGCACTCCGCGACAGGTGTCCTCTGTATCTTATCGAGTTTATGCTTGAGCTGCCTCCRG	6030
BDV JCTC.....C.....T.....	6030
BDV BrieseG.....G.....A.....	6030
Consensus	CAATCATGCAGGAYGAGTCGCTRTTACGACCCCTCTGYCTCGTAGGYCCATCCATTGGTGGGCTTCCRACYCCCTGCAACCCCTGCCAGTG	6120
BDV JCTC.....G..A.....T.....T.....A..T.....G.....	6120
BDV BrieseT.....A..G.....C.....C.....G..C.....A.....	6120
Consensus	TCTTTTTCAGAGGAATGTCGACCCCAATGCCCTTTCAGCTAGCACTCTTGAGACCCCTCATTAAACGACAGGGGTGACYTGTAGCTTGG	6210
BDV JCTT.....C.....	6210
BDV BrieseA.....G.....C.....	6210
Consensus	TGATCGTGTGTYAAGTTACGGATAGCACCCCTATCCAGACTGGCTCTCYCTAGTGACTGACCCGACYTCACCTCAACATTGCYCARGTGT	6300
BDV JCTT.....C.....C.....T.....T.....T..G.....	6300
BDV BrieseC.....T.....C.....C.A.....	6300
Consensus	ACCGGCCAGACGTCARATCAGGAGGTGGATTGAGGARGCRATAGCRACAGCTCACACTCGTCACGCATAGCAACTTTTTCAGCAGS	6390
BDV JCTA.....G.....A.....A.....	6390
BDV BrieseG.....A..G.....G.....C.....C.....	6390

FIG. 21

Consensus	CCCTCAGGAGATGGCYCAGTGCCTTGGAGGGACCTYTCAACAATGATGCCCTCTTCGRCCCGGATATGTGGCCCTATTCCGATTAT	6480
BDV JCTC...C.....C.....G.....	6480
BDV BrieseT...T.....T.....A.....	6480
Consensus	CRAATGCGCATAYGGTYTAGCATTATAGATCATTTCAAARTCCTTACCGTTGTYTCTGCAAGTCAAGCTGTCCATATCGARGATG	6570
BDV JCTT...C.....G.....C.....A.....	6570
BDV BrieseC...T.....A.....T.....G.....	6570
Consensus	TTCCCCTAGAGAGTGTAGGTATAAGGAATCTATCATYCAAGGTCTGTAGACACYACTGAGGGGTAYAACATGCAACCTTATTGGAAAG	6660
BDV JCTT.....T.....C.....T.....C.....	6660
BDV BrieseC.....C.....C.....T.....T.....	6660
Consensus	GTTGCACTTACCTTGCAGCCAARCAAGYTAGCKAGGTTGACRTGGGGTGGAGAGCTAGTTGGAGTYACAATGCCGTTTGTTCGCCAGCAAT	6750
BDV JCTG...C...G.....G.....T.....C.....	6750
BDV BrieseA...T...T.....A.....C.....	6750
Consensus	TCCATCCYCAAGTTCGTSGTGCAAAACRCRGAACCTCTACCTCGAYGCTATYATATACTGCCCCACARGAGACRTTGGCGTCACACCATC	6840
BDV JCTC...T.....C.....A...A.....T...C.....A...G.....	6840
BDV BrieseT...C.....G...G...G.....C...T.....G...A.....	6840
Consensus	TGACTACCAAGGGGACAGCGCTTTACCTYGGATCYAATACGGCTGTCCAMGGTYCAGCGAGGTGAGATCACRGGCCTTAACAAAGTCAA	6930
BDV JCTT...T.....C...T.....C...T.....A.....G.....	6930
BDV BrieseC...C.....C...A...C.....G.....	6930
Consensus	GGGCTGCAATCTAGTCARGACACTCTCGTTCTCCAYCAGTGGTAYAARGTCCGTAARGTTACCGATCCACACTTGAACACYCTCATGG	7020
BDV JCTA.....A.....C.....C...G.....G.....T.....	7020
BDV BrieseG.....G.....T.....T...A.....A.....C.....	7020
Consensus	CRGCTTCTTCTTGTGAGAGGRTACACATCTGACGCTCGRCCTAGATYCAGGGTGGACCCCTCACRCATCGTCTCCCATCCCGYGAG	7110
BDV JCT	.G.....G.....A.....A.....G.....T.....C.....A.....T.....	7110
BDV Briese	.A.....A.....G.....A.....C.....G.....G.....C.....	7110

FIG. 2J

Consensus	ACTCAGCARGGGTYACTGGGTATGTRAAATATACCTAGYACCTGGCTTCACAGTATATCTTCACACTCTTCTCGAAATCAT	7200
BDV JCTC..A.....C.....G.....C..C.....C..G.....	7200
BDV BrieseG..G.....T.....A.....A..T.....T..A.....	7200
Consensus	CAGAYGACTAYACAATCCACTTYCAGCATGTATTACACATACGGTTGCCTCTATGCTGATTGGTATAGATCGGGCGGTATTATTTCCA	7290
BDV JCTT.....C.....	7290
BDV BrieseC.....T.....	7290
Consensus	CTCCTTACCTTTTGAGTGCAGTTGTAAACATGCTTTGAGAAAGATAGACTCAGAGAGKTCGCTGGCATGYGAACCYCAATAYAGGG	7380
BDV JCTG.....G.....G.....G.....G.....	7380
BDV BrieseT.....T.....T.....T.....T.....C.....	7380
Consensus	GTGCTGAGTGGCTGATATCAAGCCAGTYACTGTCCTCGAGCAGATAATGAYGCTGAAGTCGAGTTTGACCCCTGTGTGAGTGGCGGTT	7470
BDV JCTT.....T.....T.....C.....	7470
BDV BrieseC.....C.....T.....	7470
Consensus	ATTGCTCTGGGATTCTCATTGGCAAGTCATTCTTTRGTTGACATAAGGCAAGTGGGCATGATATATGAGCAGCGGACATGGGCTAACY	7560
BDV JCTG.....G.....G.....G.....G.....	7560
BDV BrieseA.....A.....C.....	7560
Consensus	TGGAGAGGTTTCTGTRTCGGACATGCAGAAACTTCCTRTGGAGTATTGTAATTCGGTCTCTCTGGAGATTCCCTTATTGGCGCAGRCCTCC	7650
BDV JCTG.....G.....A.....A.....G.....	7650
BDV BrieseA.....A.....G.....	7650
Consensus	TYCAGTTTCAGRAGGCTGGCTYATTAGTATGCTGCTATGCTGCRACAGGTCCCAACCCYTAGCTTCCTAATGAAAGTYTTTCAAGACTCAG	7740
BDV JCTT.....G.....A.....A.....G.....	7740
BDV BrieseC.....C.....A.....CC.....	7740
Consensus	CCCTMCTYATGGACTCGGCACCCTYGTGATCGGGCTGTMCCTAGGATCAACTTTTCATAGTCGGGGAGACCTCGTGYGCYAAAGCTYGTTTTAT	7830
BDV JCTA..T.....T..T.....A.....	7830
BDV BrieseC..C.....C..C.....C.....T..T.....T.....	7830

FIG. 2K

Consensus	7920
BDV JCT	7920
BDV Briese	7920
TRCCCTTCATCAACCCGGGTATAGTGAGATTGAAGTGTCTGTRGAATTAATAGCAAGTAYCATGCACTATCGGAGCCYAAATATGATCTGT .A.....A.....T.....T..... .G.....G.....C.....C.....	
Consensus	8010
BDV JCT	8010
BDV Briese	8010
ACATCGCTGCTGMAARTCTGTGGCGTAAAGCCACACAGTTTGTGTGAGGAAACAAACAGACTTTACGGCCCGCGCCACCACCATGTTA.....A.....C.....G.....	
Consensus	8100
BDV JCT	8100
BDV Briese	8100
GTTATCCCTTCTTGGTCTAAGTCACGCAATCAATCACAGGTCCTAAAGATGGTAGTCRGGAAAGCTGAAGCTMTGTGTCCTGTATATATA.....G.....A.....A.....A.....C.....	
Consensus	8190
BDV JCT	8190
BDV Briese	8190
ACCCCACAGTCGATCCCGCGTGTCTCGACCTGTGCCAYCTGCCAGCACTAATAATCCTACTGCTCGGCGGTGACCCAGCGTACTC.....C.....C.....T.....T.....	
Consensus	8280
BDV JCT	8280
BDV Briese	8280
AYGAGCGATTACTTGAGATGGACCTRTGCGGGGTGTGTCAAAGTCGMGTGATATCCCCCATTCYCTRGCTGSCAGAACGCCAGGGGGT .C.....A.....C.....C.....C..... .T.....G.....A.....A.....T.....G.....	
Consensus	8370
BDV JCT	8370
BDV Briese	8370
TCRCARTRGGCCAGACGCTGTGTCAGGTGTRATTAGACTYGCACARGTTAGAGTCRGTTTGTGTAYGCYACACCCCTGTTTRGAGGARCTAG ..A..A.....G.....T.....G.....C.....C.....G..... ..G..G.....A.....C.....G.....A.....T.....T.....A.....A.....	
Consensus	8460
BDV JCT	8460
BDV Briese	8460
AGTTTATGCRATYCTAGACTCTGAGTTRGTTGAYATTAGTGATATGTGCTGCCCTCCCVTAGCCACACCCCTGTAAGCCCTWTTTCAGGCG..C.....A.....T.....C.....C.....A.....A..T.....G.....C.....T.....T.....	
Consensus	8550
BDV JCT	8550
BDV Briese	8550
CARTRTATCGGAGCTTACAGTCGTTACAGTTAGCCTTAATGGACAACACTATAGTTTGTMTATGGACCTCATTAYCATCCGGRGRSTGGACA ..G..G.....A.....C.....C.....G.....G..... ..A.....A.....T.....T.....A.....AC.....	

FIG. 2L

Consensus	8640
BDV JCT	8640
BDV Briese	8640
<p> TYAGCCTCACCTGAGGARTTGTGAGCTGCTGTGTRGRCAGCAYATCCTCGGYCAGCCCGTCCCTAGTRGAGGTTGTTACTACG .C.....G....T.A.....G.G....T.....T.....G..... .T.....A.....C.G.....A.A.....C.....C.....A..... </p>	
Consensus	8730
BDV JCT	8730
BDV Briese	8730
<p> TTGGAGTTGTRGGAAGGCTGTGTTAGCGAGGCATCCSTGGTCAGCAGATCTTAAGCGAATYACTGTRGGGGGGCGKCCCTGCC G.....T.....C.....C.....A.....A.G..... A.....C.....G.....T.....G.....G.T..... </p>	
Consensus	8820
BDV JCT	8820
BDV Briese	8820
<p> CYTCTGCTGCGYRGATGCGGTGATGAGGATTGTCRGGGGTCTCTGTGTTGGCTTCCTGCTGRTTGACGCACTTTRTGTGRTTGTAT .T.....TG.C.....G.....C.....A.....A.....G.....G.G..... .C.....CA.T.....A.....T.....T.....G.....A.....A.AA..... </p>	
Consensus	8910
BDV JCT	8908
BDV Briese	8910
<p> RAGRTYRAGCCAYCTACRCCCTATTCTTAAAAAACCATAYGTCAGTGCTGGGTTGGTTGCTTTGCTTTGTTGTAGCGCKTT G..G.TG....T...G.....C.....T.....T.....T--- A..A.CA....C....A.....T.....C.....G..... </p>	

FIG. 2M

FIG 3A

FIG 3B

C H1 H2 H3 M (bp)



	10	20	30	40	50	60	70	80	90	100	
Strain V	ATGGCAACCGGACCATCGAGTCTGGTCCCTGGAGGACGAGAAGATCCCCAGACACTACGACGGGAACGACCCGGGTCA	CCCAAGG	ATCGAGTCTGGTCCCTGGAGGACGAGAAGATCCCCAGACACTACGACGGGAACGACCCGGGTCA	CCCAAGG	ATCGAGTCTGGTCCCTGGAGGACGAGAAGATCCCCAGACACTACGACGGGAACGACCCGGGTCA	CCCAAGG	ATCGAGTCTGGTCCCTGGAGGACGAGAAGATCCCCAGACACTACGACGGGAACGACCCGGGTCA	CCCAAGG	ATCGAGTCTGGTCCCTGGAGGACGAGAAGATCCCCAGACACTACGACGGGAACGACCCGGGTCA	CCCAAGG	ATCGAGTCTGGTCCCTGGAGGACGAGAAGATCCCCAGACACTACGACGGGAACGACCCGGGTCA
H1	GA	100
H2	GA	100
H3	GA	100
C6BV	GA	100
	110	120	130	140	150	160	170	180	190	200	
Strain V	TCCCAAGGAATGATTGACCCCAACCAAGTACAGCAGCTCCTGAAGGACCTCAGGAAGACCCCTCCATGATCTCAGACCCAGACCCGGAACCCGGAAGGGA										200
H1	200
H2	200
H3	200
C6BV	200
	210	220	230	240	250	260	270	280	290	300	
Strain V	GCAGCTGTGGAATGATGAGCTAATCAAGAAGTTAGTGACGGAGCTGGCCGAGAATAGCATGATCGAGGCTGAGGAGGTGCGGGGCACTCTTGGAGACATC										300
H1	300
H2	300
H3	300
C6BV	300
	310	320	330	340	350	360	370	380	390	400	
Strain V	TCGGCTCGTATCGAGGCAAGGTTTGAGTCCCTGTCCGCCCTCCCAAGTGGAAACCATCCAGACAGCTCAGCGGTGCGGATCACTCCGACAGCATCAGGATCC										400
H1	400
H2	400
H3	400
C6BV	400

FIG. 4A-I

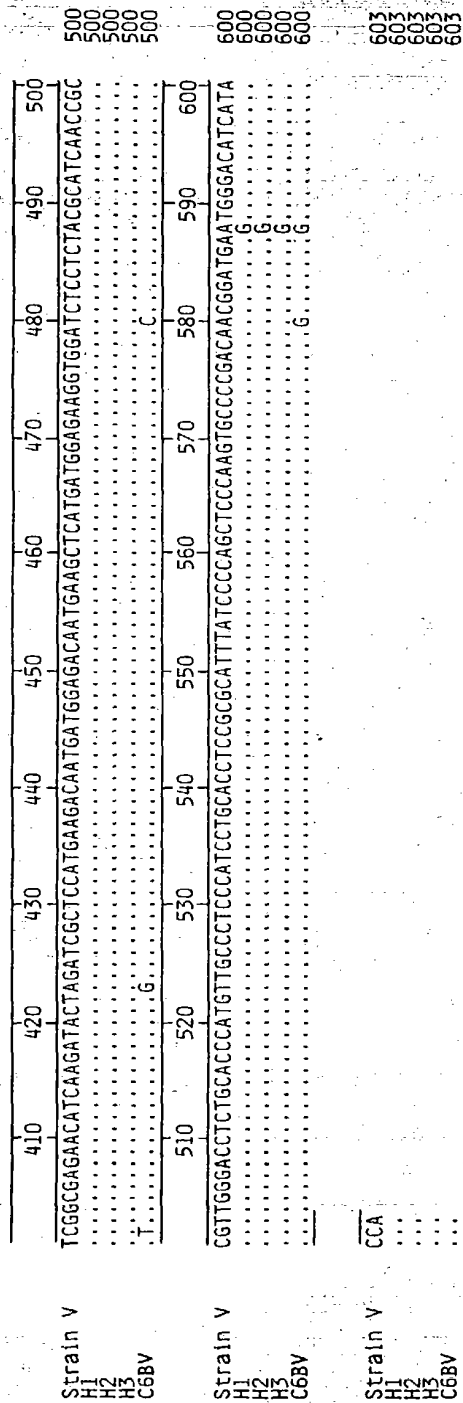


FIG. 4A-2

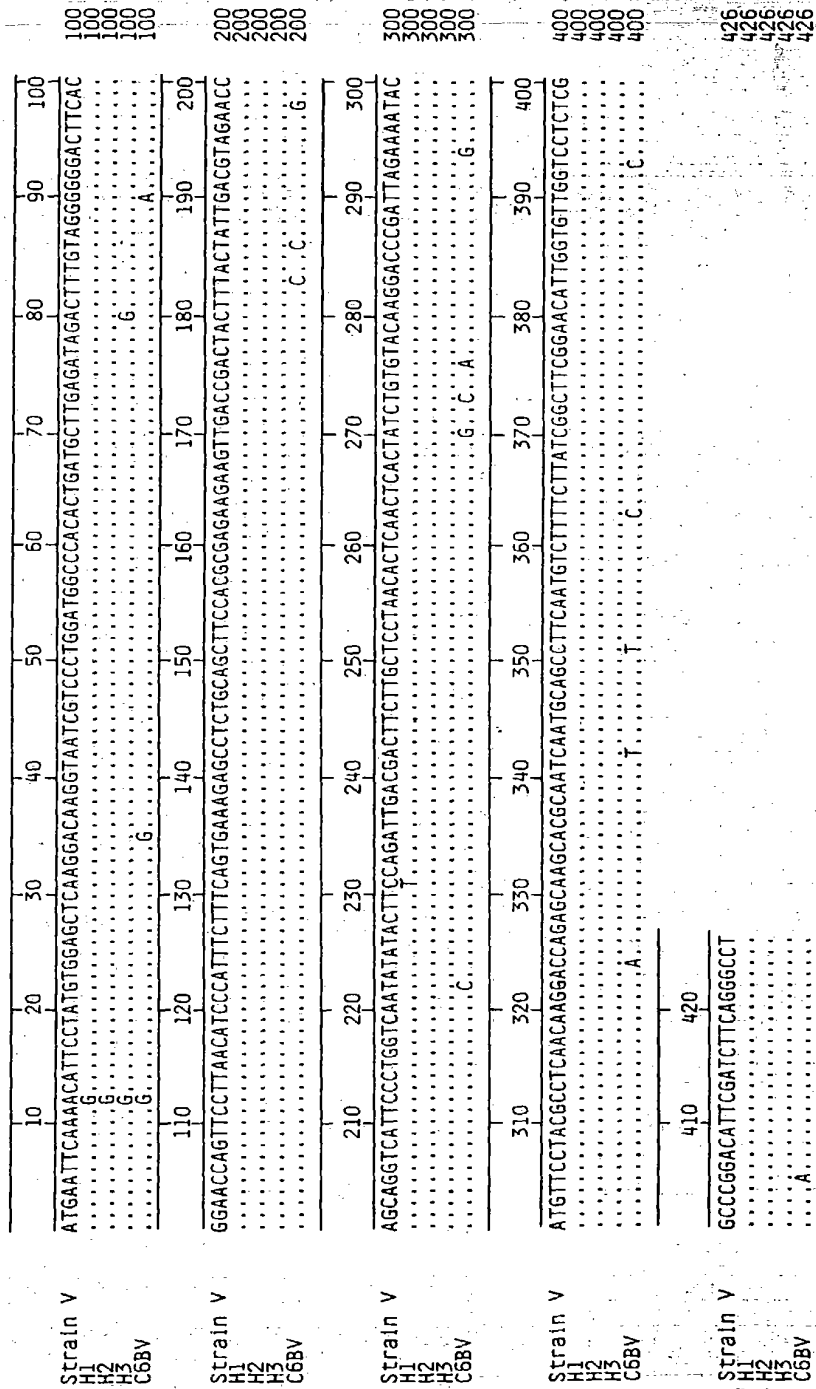


FIG. 4B

Strain V	10	20	30	40	50	60	70	80	90	100	100
H1	ATGCAGCCTTCAATGCTCTTTCTTATCGGCTTCGGACATGGGTGGTCTCTCGGCCGGACATCGATCTTCAGGGCCTTAGCTGCAATACTGACT										100
H2										100
H3										100
C68VT.....C.....C.....A.....T.....										100
Strain V	110	120	130	140	150	160	170	180	190	200	200
H1	CCACTCTGGACTGATTGACCTGGAGATAGGGGACTTTGCCACACCCCAAGGAAATGTCTTCATTCGCGAGTTAGTTATCTCAACCCACACGACTAT										200
H2										200
H3										200
C68VT.A..C..T.....										200
Strain V	210	220	230	240	250	260	270	280	290	300	300
H1	TAGCTCCGGCAGTCCACACATCATGCTCAAGTACCACTGCAAAACCTATTGGGATTCCTTTGGTAGCTACAGCGCTGACCGAATCATAAATCGGTAC										300
H2										300
H3										300
C68V6.....										300
Strain V	310	320	330	340	350	360	370	380	390	400	400
H1	ACTGCTACTGTTAAGGGTTGCTTAACAACTCAGCACAGAGAGCCCTTCGAGTGCACCTGTTCTACTGCTGCTCGGCGATTACAACAGAGATCTGCC										400
H2										400
H3										400
C68VT.....6.....T.....										400
Strain V	410	420	430	440	450	460	470	480	490	500	500
H1	GATGCTCTATTACAAATGTCAGGGTGGCTGTGCAAACTTCCACCCTTCATGTACTGCAGCTTTCGAGACTGCGAGTACCCTGAGCCCAACAGGAGCTAGA										500
H2										500
H3										500
C68VA..6.....C..6.....T.....T.....G.....										500
Strain V	510	520	530	540	550	560	570	580	590	600	600
H1	GAGTGGAAAGGCAATGCTGAGCGATGGCAGTACATTAACTTATACCCGTATATCTACAGTCAGAGTGTGAACAAACCCCTCAATGGGACCATACTC										600
H2										600
H3										600
C68VC.....C.....T.....A.....T.....T.....T.....										600

FIG. 4C-I

Strain V	610	620	630	640	650	660	670	680	690	700
H1	TGCACTCATCCTCTAAGATAGTTTCTTCGATGAATTTAGGCGTTTCATCTCCCTAAGAAATGGTAGTTACCGAGGCTCATCAATCAATGTGACGTGTG									700
H2									700
H3									700
C6BVC.....			G.....					700
Strain V	710	720	730	740	750	760	770	780	790	800
H1	CAAACTACACGTCGTCCTGCGGCGCCAGGTTGAAAAGGCGGCGTAGGGACACCCAGCAGATTGAGTATCTAGTTCACAAGCTTAGGCCCACTGAAAGA									800
H2									800
H3									800
C6BVT.....T.....A.....G.....T.....T.....A.....C.....									800
Strain V	810	820	830	840	850	860	870	880	890	900
H1	TGCATGGGAGGACTGTGAGATCCTCCAGTCTCTGCTCCTAGGGGTTTGGTACTGGGATCGCAAGTCTTCTCAATTTTGAGGAGCTGGCTCAACAC									900
H2									900
H3									900
C6BVG.....T.....A.....T.....G.....C.....G.....									900
Strain V	910	920	930	940	950	960	970	980	990	1000
H1	CCTGACATCATCGGGTATAGTTAATGGAGTTGGGGTTGTCTGGCAATGCCATCGTGTTAATGTCAAGTTCATGGCGTGGAAATGAGTCCACCTATTACC									1000
H2									1000
H3									1000
C6BVT.....A.....A.....A.....A.....A.....A.....A.....									1000
Strain V	1010	1020	1030	1040	1050	1060	1070	1080	1090	1100
H1	CTCCAGTAGATTACAATGGCGGAAGTACTTCTCGAATGATAGGGAAGGTTACACAAACACCCCGAGGCAAGGCCAGGGCTTAAGCGGGTCATGTG									1100
H2									1100
H3									1100
C6BVA.....T.....T.....G.....C.....									1100
Strain V	1110	1120	1130	1140	1150	1160	1170	1180	1190	1200
H1	GTTGGCAGGTACTTCTAGGGACAGTAGGGTCTGGGGTGAACCGAGGAGGATTCGGTACATAAAGACCTCACATGACTACCACTGGAGGAGTTTGAG									1200
H2									1200
H3									1200
C6BVT.....T.....T.....T.....T.....T.....T.....									1200

FIG. 4C-2

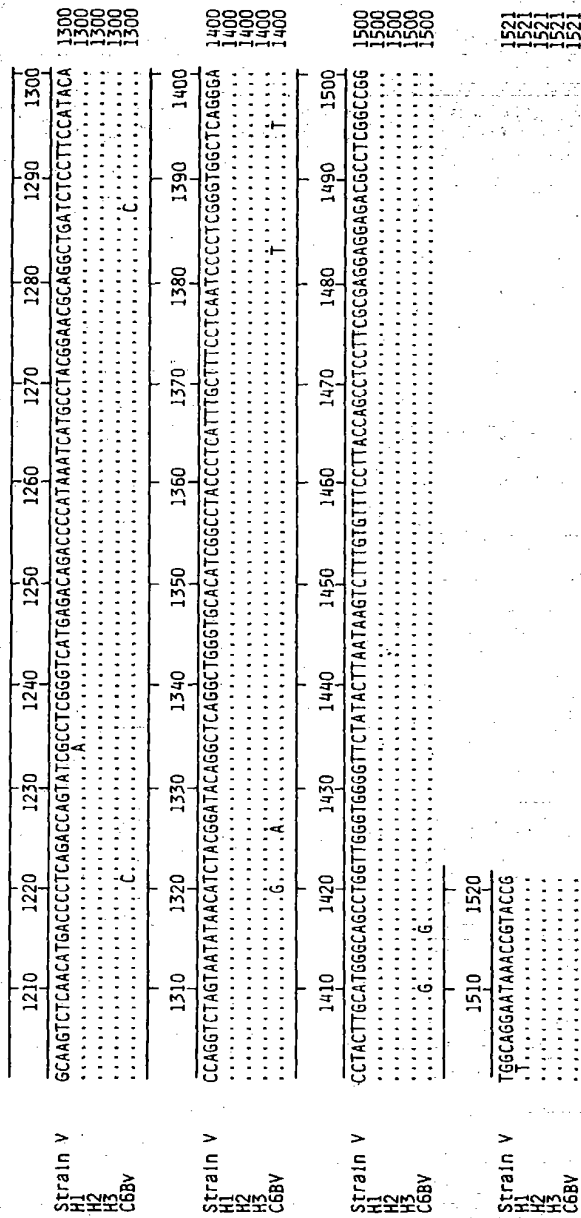


FIG. 4C-3

C6BV p40IntC.....	50
H1 p40IntC.....	50
H2 p40IntC.....	50
H3 p40IntC.....	50
StrainV p40IntT.....	50
Consensus	TTCATACAGT AACGCCAGC CTTGTGTTTC TATGTTTGCT AATCCCAGGA	50
C6BV p40IntC.....	100
H1 p40IntC.....	100
H2 p40IntC.....	100
H3 p40IntC.....	100
StrainV p40IntC.....	100
Consensus	CTGCACGCTG CGTTTGTTCA CGGAGGGGTG CCTCGTGAAT GTTACCTGTC	100
C6BV p40IntG.....	150
H1 p40IntG.....	150
H2 p40IntG.....	150
H3 p40IntG.....	150
StrainV p40IntG.....	150
Consensus	GACGCCCTTTC ACGCGTGGRG AACAGACTGT YGTTAAGACT GORRAGTTTT	150
C6BV p40IntA.....	200
H1 p40IntA.....	200
H2 p40IntA.....	200
H3 p40IntA.....	200
StrainV p40IntA.....	200
Consensus	ACGGGGAAAA GACRACRAG CGTGATCTCA CCGAGCTGGA GATCTCCTCT	200
C6BV p40IntA.....	250
H1 p40IntA.....	250
H2 p40IntA.....	250
H3 p40IntA.....	250
StrainV p40IntA.....	250
Consensus	ATTTTCAGCC ATTGTTGCTC ATTACTAAAT GGGGTTGTGA TAGGATCGTC	250
C6BV p40IntT.....	300
H1 p40IntT.....	300
H2 p40IntT.....	300
H3 p40IntT.....	300
StrainV p40IntT.....	300
Consensus	RTCTAAGATY AAAGCAGTAG CCGAGCAGAT CAAGAAAAGG TTTAAACTA	300

FIG. 5A-1

FIG. 5A-2

Consensus	TGACCATGAG CTCAACGGY CTAACCAAC TTCTTAACCG GCTATCACAT	50
p180fragC.....C.....T.....	50
H1 p180T.....C.....	50
H2 p180T.....C.....	50
H3 p180T.....C.....	50
Strain 5 p180T.....C.....	50
Consensus	ACTATCACTA AGGGTGACTC CTTTGTATT AAQYMGAY ATAGTCCTG	100
p180fragT..A..T..C.....	100
H1 p180C..T..C.....	100
H2 p180C..T..C.....	100
H3 p180C..T..C.....	100
Strain 5 p180C..T..C.....	100
Consensus	GTGCAACGGT TTCCGACCAG AACTCARGC CCCATCTGT CGTCAGTTGG	150
p180fragA..A.....C.....	150
H1 p180G..G.....A.....	150
H2 p180G..G.....A.....	150
H3 p180G..G.....A.....	150
Strain 5 p180G..G.....A.....	150
Consensus	ATCAGATGTT CAATTGCGGG TACTTCTTCA GGACTGGGTG CACACTGCCA	200
p180frag	200
H1 p180	200
H2 p180	200
H3 p180	200
Strain 5 p180	200
Consensus	TGCTTTACCA CGTTTATTAT TCARGACAGR TTCAACCCGC CCTATTCCT	250
p180fragG.....A.....T.....	250
H1 p180A.....G.....C.....	250
H2 p180A.....G.....C.....	250
H3 p180A.....G.....C.....	250
Strain 5 p180A.....G.....C.....	250
Consensus	CTGTGGTGAG CCCGTTGAAG ACGGCTTAC ATGCGCGGTT GGGACTAARA	300
p180fragC.....T.....C.....G.....	300
H1 p180A.....A.....T.....A.....	300
H2 p180A.....A.....T.....A.....	300
H3 p180A.....A.....T.....A.....	300
Strain 5 p180A.....A.....T.....A.....	300

FIG. 5B-1

Consensus	CAATGGGGA GGGATGAGG CAGAACTAT GGACAATCT TACGAGCTGC	350
p180fragA.....T.....T.....	350
H1 p180G.....C.....C.....	350
H2 p180G.....C.....C.....	350
H3 p180G.....C.....C.....	350
Strain 5 p180G.....C.....C.....	350
Consensus	TGGGAGATAA TTGCTCTTCG GGAAATTAAC GTGACGTTA AATACTAGG	400
p180fragT.....C.....C.....	400
H1 p180T.....C.....C.....	400
H2 p180T.....C.....C.....	400
H3 p180T.....C.....C.....	400
Strain 5 p180T.....C.....C.....	400
Consensus	CCARGGTGAT AATCAGACAA TCATYRTACA TAAATCTGCA AGCCAAAATA	450
p180fragG.....TG.....	450
H1 p180A.....CA.....	450
H2 p180A.....CA.....	450
H3 p180A.....CA.....	450
Strain 5 p180A.....CA.....	450
Consensus	ATCAGCTATT AGCGGAGCGA GCATYRGGG GYMTGTACAA GCATGCTAGA	500
p180fragT.....G.....A.....TT.....	500
H1 p180C.....C.....G.....CC.....	500
H2 p180C.....C.....G.....CC.....	500
H3 p180C.....C.....G.....CC.....	500
Strain 5 p180C.....C.....G.....CC.....	500
Consensus	TTAGCTGGCC ATAACCTTAA GGTAGARGAA TGYTGGGTGT CAGATTGTCT	550
p180fragT.....A.....T.....	550
H1 p180C.....G.....C.....	550
H2 p180C.....G.....C.....	550
H3 p180C.....G.....C.....	550
Strain 5 p180C.....G.....C.....	550
Consensus	GTATGAGTAT GGAAAGAAGC TTTCTTCCG TGGTGTACCT GTCCCGGCT	600
p180fragC.....A.....	600
H1 p180T.....G.....	600
H2 p180T.....G.....	600
H3 p180T.....G.....	600
Strain 5 p180T.....G.....	600

FIG. 5B-2

Consensus	GTITGAAGCA GCTCTGCGG GTGACGGAT CACTGGGCA GYATTCCTCA	650
p180fragG.....C.....G.....T.....	650
H1 p180A.....T.....A.....C.....	650
H2 p180A.....T.....A.....C.....	650
H3 p180A.....T.....A.....C.....	650
Strain 5 p180A.....T.....A.....C.....	650

Consensus	AACCTATACT CAAAGTTAGC CTGCTAACCA TCATORTGY	689
p180fragT.....A.....C.....	689
H1 p180T.....A.....C.....	689
H2 p180T.....A.....C.....	689
H3 p180T.....A.....C.....	689
Strain 5 p180T.....A.....C.....	689

FIG. 5B-3

p24				p16				p56															
4	26	34	127	194	12	27	108	3	7	17	21	220	234	242	243	245	282	296	326	412	465	501	
C6BV	G	S	I	H	A	G	D	E	L	S	A	Q	A	V	S	L	R	M	G	A	A	L	W
H1	E	-	V	Y	T	D	-	D	P	F	V	R	T	A	P	R	L	V	S	T	T	P	L
H2	-	-	V	-	T	-	-	D	P	F	V	R	T	A	P	R	L	V	S	T	-	-	-
H3	E	-	V	-	T	-	G	D	P	F	V	R	T	A	P	R	L	V	S	T	-	P	-
Strain V	R	P	V	-	T	D	-	D	P	F	V	R	T	A	P	R	L	V	S	-	-	P	-

FIG. 6A

p24					p16					p56				
C6BV	H1	H2	H3	Strain V	C6BV	H1	H2	H3	Strain V	C6BV	H1	H2	H3	Strain V
	16	14	14	17		17	16	17	16		67	65	65	64
C6BV	4	2	1	5		2	2	3	3	15	2	2	2	3
H1														
H2	2	2	2	3	1	1	1	1	1	13	2	0	0	1
H3	3	1	1	5	2	2	1	2	2	13	2	0	0	1
Strain V	4	3	2	2	1	1	0	1	1	12	3	1	1	1

FIG. 6B

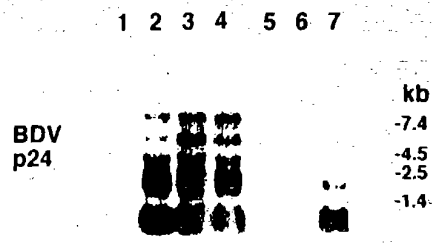


FIG. 7A

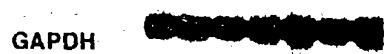


FIG. 7B

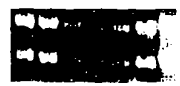


FIG. 7C

MATEPSSLVDSLEDEEDPQTLRRERSGSPRPRKVPVRNALTQPVQDQLLKDLRKNPSMISDP
DQRTGREQLSNDELIKLLVTELAENSMIEAEVVRGTLGDISARIEAGFESLSALQVETIQT
AQRCDSIRILGENIKILDRSMKTMETMKLMMEKVDLLYASTAVGTSAPMLPSHP
APPRYPQLPSAPTIDEWDIIP

FIG. 8A

MATGPSSLVDSLEDEEDPQTLRRERSGSPRPRKVPVRNALTQPVQDQLLKDLRKNPSMISDP
DQRTGREQLSNDELIKLLVTELAENSMIEAEVVRGTLGDISARIEAGFESLSALQVETIQT
AQRCDSIRILGENIKILDRSMKTMETMKLMMEKVDLLYASTAVGTSAPMLPSHP
APPRYPQLPSAPTIDEWDIIP

FIG. 8B

MATEPSSLVDSLEDEEDPQTLRRERSGSPRPRKVPVRNALTQPVQDQLLKDLRKNPSMISDP
DQRTGREQLSNDELIKLLVTELAENSMIEAEVVRGTLGDISARIEAGFESLSALQVETIQT
AQRCDSIRILGENIKILDRSMKTMETMKLMMEKVDLLYASTAVGTSAPMLPSHP
APPRYPQLPSAPTIDEWDIIP

FIG. 8C

MNSKHSYVELKDKVIVPGWPTLMLEIDFVGTSRNQFLNIPFLSVKEPLQLPREKKLTDY
FTIDVEPAGHSLVNIYFQIDDFLLTLNLSVYKDPKPYMFLRLNKDQSKHAINAAFNVF
SYRLRNIGVGPLGPDIRSSGP

FIG. 9A

MNSKHSYVELKDKVIVPGWPTLMLEIDFVGTSRNQFLNIPFLSVKEPLQLPREKKLTDY
FTIDVEPAGHSLVNIYFQIDDFLLTLNLSVYKDPKPYMFLRLNKDQSKHAINAAFNVF
SYRLRNIGVGPLGPDIRSSGP

FIG. 9B

MNSKHSYVELKDKVIVPGWPTLMLEIGFVGTSRNQFLNIPFLSVKEPLQLPREKKLTDY
FTIDVEPAGHSLVNIYFQIDDFLLTLNLSVYKDPKPYMFLRLNKDQSKHAINAAFNVF
SYRLRNIGVGPLGPDIRSSGP

FIG. 9C

MQPSMSFLIGFGTLVLVSARTFDLQGLSCNTDSTPGLIDLEIRRLCHTPTENVISCEVSYL
NHTTISLPAVHTSCLKYHCKTYWGFFGSYADRINRYTGTGCLNNSAPEDPPECNW
FYCCSAITTEICRCSTNVTVAQTFPPFMYCSFADCSYVSSQEELESGKAMLDGSLTYT
PYLQSEVNVNKTNGTILCNSSSKIVSDEFRRSYSLTNGSYQSSINVTANYTSSCRPRL
KRRRDTQQIEYL VHKLRPTLKDA WEDCEILQSLLLGVFGTGIASASQFLRWLNHPDII
GYVNGVGVVWQCHRVNVTFTWNESTYYPVDYNGRKYFLNDEGRQLQNTPEARPG
LKRVMWFGRYFLGTGSGVKPRRJRYNKTSHDYHLEEFASLNMTPQTSITSGHETDPI
NHA YGTQADLLPYTRSSNITSDTGTSGVWHIGLPSFAFLNPLGWLRLDLLA WAAWLGGV
LYLISLCVSLPASFAARRRLGRQLQE

FIG. 10A

MQPSMSFLIGFGTLVLVSARTFDLQGLSCNTDSTPGLIDLEIRRLCHTPTENVISCEVSYL
NHTTISLPAVHTSCLKYHCKTYWGFFGSYADRINRYTGTGCLNNSAPEDPPECNW
FYCCSAITTEICRCSTNVTVAQTFPPFMYCSFADCSYVSSQEELESGKAMLDGSLTYT
PYLQSEVNVNKTNGTILCNSSSKIVSDEFRRSYSLTNGSYQSSINVTANYTSSCRPRL
KRRRDTQQIEYL VHKLRPTLKDA WEDCEILQSLLLGVFGTGIASASQFLRWLNHPDII
GYVNGVGVVWQCHRVNVTFTWNESTYYPVDYNGRKYFLNDEGRQLQNTPEARPG
LKRVMWFGRYFLGTGSGVKPRRJRYNKTSHDYHLEEFASLNMTPQTSITSGHETDPI
NHA YGTQADLLPYTRSSNITSDTGTSGVWHIGLPSFAFLNPLGWLRLDLLA WAAWLGGV
LYLISLCVSLPASFAARRRLGRWQE

FIG. 10B

10	20	30	40	50
1234567890	1234567890	1234567890	1234567890	1234567890
HIVTSLVFL	CLLIRGLHAA	FVHGGVPRES	YLSPTVRGE	QIVWKTAEFY
50				
GEKITQORDLT	ELEISSIFSH	CCSLLIGWVI	GSSSKIKAGA	EQIKKRFKTM
100				
MAALNRPSHG	ETATLLQMFN	PHEAIDWING	QFWGGSFVL	LLTTDFESPG
150				
KERMQIKLV	ASYAQMTT	TIKEYLAECM	DATLTIPW	
189				

FIG. IIA

10	20	30	40	50
1234567890	1234567890	1234567890	1234567890	1234567890
HIVTSLVFL	CLLIRGLHAA	FVHGGVPRES	YLSPTVRGE	QIVWKTAEFY
50				
GEKITQORDLT	ELEISSIFSH	CCSLLIGWVI	GSSSKIKAGA	EQIKKRFKTM
100				
MAALNRPSHG	ETATLLQMFN	PHEAIDWING	QFWGGSFVL	LLTTDFESPG
150				
KERMQIKLV	ASYAQMTT	TIKEYLAECM	DATLTIPW	
189				

FIG. IIB

10	20	30	40	50
1234567890	1234567890	1234567890	1234567890	1234567890
HIVTSLVFL	CLLIRGLHAA	FVHGGVPRES	YLSPTVRGE	QIVWKTAEFY
50				
GEKITQORDLT	ELEISSIFSH	CCSLLIGWVI	GSSSKIKAGA	EQIKKRFKTM
100				
MAALNRPSHG	ETATLLQMFN	PHEAIDWING	QFWGGSFVL	LLTTDFESPG
150				
KERMQIKLV	ASYAQMTT	TIKEYLAECM	DATLTIPW	
189				

FIG. IIC

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
TMSSTALTHL	LNRLSHITIK	GDSFVINLDY	SSWNGFRPE	LQAPICRQID	50
QMFNGYFFR	TGCTLECFIT	FIIQDRFNPP	YSLSGEPVED	GVTCavgIKT	100
MGEQMRQKLW	TIITSCWEII	ALREINVTFN	IIGQGINQTI	IIHKSASQNN	150
QLLAERALGA	LYKHARLAGH	NLKVEECWVS	DCLYEYGGKL	FFRGVFPVGC	200
LKQLSRVIDS	TGELFPNLVS	KLACLTSSC			229

FIG. 12